

RAW SEQUENCE LISTING

PATENT APPLICATION: US/09/765,271

DATE: 03/16/2001

TIME: 17:53:03

Input Set : N:\paola\09765271.txt

Output Set: N:\CRF3\03162001\I765271.raw

ENTERED

SEQUENCE LISTING

5 (1) GENERAL INFORMATION:
7 (i) APPLICANT: Choi et. al.
9 (ii) TITLE OF INVENTION: Streptococcus pneumoniae Antigens and Vaccines
11 (iii) NUMBER OF SEQUENCES: 452
13 (iv) CORRESPONDENCE ADDRESS:
15 (A) ADDRESSEE: Human Genome Sciences, Inc.
16 (B) STREET: 9410 Key West Avenue
17 (C) CITY: Rockville
18 (D) STATE: Maryland
19 (E) COUNTRY: USA
20 (F) ZIP: 20850
23 (v) COMPUTER READABLE FORM:
25 (A) MEDIUM TYPE: Diskette, 3.50 inch, 1.4Mb storage
26 (B) COMPUTER: HP Vectra 486/33
27 (C) OPERATING SYSTEM: MSDOS version 6.2
28 (D) SOFTWARE: ASCII Text
31 (vi) CURRENT APPLICATION DATA:
C--> 33 (A) APPLICATION NUMBER: US/09/765,271
C--> 34 (B) FILING DATE: 22-Jan-2001
35 (C) CLASSIFICATION:
38 (vii) PRIOR APPLICATION DATA:
40 (A) APPLICATION NUMBER: 09/536,784
41 (B) FILING DATE:
43 (A) APPLICATION NUMBER: 08/961,083
44 (B) FILING DATE: OCT-30-1997
47 (viii) ATTORNEY/AGENT INFORMATION:
49 (A) NAME: Michelle S. Marks
50 (B) REGISTRATION NUMBER: 41,971
51 (C) REFERENCE/DOCKET NUMBER: PB340P3
C--> 54 (ix) TELECOMMUNICATION INFORMATION:
56 (A) TELEPHONE: (301) 309-8504
57 (B) TELEFAX: (301) 309-8512
60 (2) INFORMATION FOR SEQ ID NO: 1:
62 (i) SEQUENCE CHARACTERISTICS:
63 (A) LENGTH: 1999 base pairs
64 (B) TYPE: nucleic acid
65 (C) STRANDEDNESS: double.
66 (D) TOPOLOGY: linear
69 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1:
71 TAAAATCTAC GACAATAAAA ATCAACTCAT TGCTGACTTG GGTCTCTGAAC GCCGCGTCAA 60
73 TGCCCAAGCT AATGATATTC CCACAGATTT GGTAAAGGCA ATCGTTTCTA TCGAAGACCA 120
75 TCGCTTCTTC GACCACAGGG GGATTGATAC CATCCGTATC CTGGGAGCTT TCTTGCGCAA 180
77 TCTGCAAAGC AATTCCCTCC AAGGTGGATC AACTCTCACC CAACAGTTGA TTAAGTTGAC 240
79 TTAATTTTCA ACTTCGACTT CCGACCAGAC TATTTCTCGT AAGGCTCAGG AAGCTTGGTT 300
81 AGCGATTTCAG TTAGAACAAA AAGCAACCAA GCAAGAAATC TTGACCTACT ATATAAATAA 360
83 GGTCTACATG TCTAATGGGA ACTATGGAAT GCAGACAGCA GCTCAAACT ACTATGGTAA 420

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```

85 AGACCTCAAT AATTAAAGTT TACCTCAGTT AGCCTTGCTG GCTGGAATGC CTCAGGCACC      480
87 AAACCAATAT GACCCCTATT CACATCCAGA AGCAGCCCAA GACCGCCGAA ACTTGGTCTT      540
89 ATCTGAAATG AAAAATCAAG GCTACATCTC TGCTGAACAG TATGAGAAAG CAGTCAATAC      600
91 ACCAATTACT GATGGACTAC AAAGTCTCAA ATCAGCAAGT AATTACCCTG CTTACATGGA      660
93 TAATTACCTC AAGGAAGTCA TCAATCAAGT TGAAGAAGAA ACAGGCTATA ACCTACTCAC      720
95 AACTGGGATG GATGTCTACA CAAATGTAGA CCAAGAAGCT CAAAAACATC TGTGGGATAT      780
97 TTACAATACA GACGAATACG TTGCCTATCC AGACGATGAA TTGCAAGTCG CTTCTACCAT      840
99 TGTGATGTT TCTAACGGTA AAGTCATTGC CCAGCTAGGA GCACGCCATC AGTCAAGTAA      900
101 TGTTTCCTTC GGAATTAACC AAGCAGTAGA AACAAACCGC GACTGGGGAT CAACTATGAA      960
103 ACCGATCACA GACTATGCTC CTGCCTTGGA GTACGGTGTC TACGATTCAA CTGCTACTAT     1020
105 CGTTCACGAT GAGCCCTATA ACTACCCTGG GACAAATACT CCTGTTTATA ACTGGGATAG     1080
107 GGGCTACTTT GGCAACATCA CCTTGCAATA CGCCCTGCAA CAATCGCGAA ACGTCCAGC     1140
109 CGTGGAAACT CTAAACAAGG TCGGACTCAA CCGCGCCAAG ACTTTCCTAA ATGGTCTAGG     1200
111 AATCGACTAC CCAAGTATTC ACTACTCAAA TGCCATTTC AAGTAACACAA CCGAATCAGA     1260
113 CAAAAAATAT GGAGCAAGTA GTGAAAAGAT GGCTGCTGCT TACGCTGCCT TTGCAAATGG     1320
115 TGGAACTTAC TATAAACCAA TGTATATCCA TAAAGTCGTC TTTAGTGATG GGAGTGAAAA     1380
117 AGAGTTCTCT AATGTCGGAA CTCGTGCCAT GAAGGAAACG ACAGCCTATA TGATGACCGA     1440
119 CATGATGAAA ACAGTCTTGA CTTATGGAAC TGGACGAAAT GCCTATCTTG CTTGGCTCCC     1500
121 TCAGGCTGGT AAAACAGGAA CCTCTAACTA TACAGACGAG GAAATTGAAA ACCACATCAA     1560
123 GACCTCTCAA TTTGTAGCAC CTGATGAAC TTTTGTGGC TATACGCGTA AATATTCAAT     1620
125 GGCTGTATGG ACAGGCTATT CTAACCGTCT GACACCACTT GTAGGCAATG GCCTTACGGT     1680
127 CGTGCCCAA GTTTACCGCT CTATGATGAC CTACCTGTCT GAAGGAAGCA ATCCAGAAGA     1740
129 TTGGAATATA CCAGAGGGGC TCTACAGAAA TGGAGAATTC GTATTTAAAA ATGGTGCTCG     1800
131 TTCTACGTGG AACTCACCTG CTCCACAACA ACCCCATCA ACTGAAAGT CAAGCTCATC     1860
133 ATCAGATAGT TCAACTTCAC AGTCTAGTCA AACCACCTCA AGCACAATA ATAGTACGAC     1920
135 TACCAATCCT AACAATAATA CGCAACAATC AAATACAACC CCTGATCAAC AAAATCAGAA     1980
137 TCCTCAACCA GCACAACCA                                     1999

```

139 (2) INFORMATION FOR SEQ ID NO: 2:

141 (i) SEQUENCE CHARACTERISTICS:

142 (A) LENGTH: 666 amino acids

143 (B) TYPE: amino acid

144 (C) STRANDEDNESS: single

145 (D) TOPOLOGY: linear

147 (ii) MOLECULE TYPE: protein

150 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2:

```

152 Lys Ile Tyr Asp Asn Lys Asn Gln Leu Ile Ala Asp Leu Gly Ser Glu
153 1 5 10 15
155 Arg Arg Val Asn Ala Gln Ala Asn Asp Ile Pro Thr Asp Leu Val Lys
156 20 25 30
158 Ala Ile Val Ser Ile Glu Asp His Arg Phe Phe Asp His Arg Gly Ile
159 35 40 45
161 Asp Thr Ile Arg Ile Leu Gly Ala Phe Leu Arg Asn Leu Gln Ser Asn
162 50 55 60
164 Ser Leu Gln Gly Gly Ser Thr Leu Thr Gln Gln Leu Ile Lys Leu Thr
165 65 70 75 80
167 Tyr Phe Ser Thr Ser Thr Ser Asp Gln Thr Ile Ser Arg Lys Ala Gln
168 85 90 95
170 Glu Ala Trp Leu Ala Ile Gln Leu Glu Gln Lys Ala Thr Lys Gln Glu
171 100 105 110

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173   Ile Leu Thr Tyr Tyr Ile Asn Lys Val Tyr Met Ser Asn Gly Asn Tyr
174           115                      120                      125
176   Gly Met Gln Thr Ala Ala Gln Asn Tyr Tyr Gly Lys Asp Leu Asn Asn
177           130                      135                      140
179   Leu Ser Leu Pro Gln Leu Ala Leu Leu Ala Gly Met Pro Gln Ala Pro
180           145                      150                      155                      160
182   Asn Gln Tyr Asp Pro Tyr Ser His Pro Glu Ala Ala Gln Asp Arg Arg
183           165                      170                      175
185   Asn Leu Val Leu Ser Glu Met Lys Asn Gln Gly Tyr Ile Ser Ala Glu
186           180                      185                      190
188   Gln Tyr Glu Lys Ala Val Asn Thr Pro Ile Thr Asp Gly Leu Gln Ser
189           195                      200                      205
191   Leu Lys Ser Ala Ser Asn Tyr Pro Ala Tyr Met Asp Asn Tyr Leu Lys
192           210                      215                      220
194   Glu Val Ile Asn Gln Val Glu Glu Glu Thr Gly Tyr Asn Leu Leu Thr
195           225                      230                      235                      240
197   Thr Gly Met Asp Val Tyr Thr Asn Val Asp Gln Glu Ala Gln Lys His
198           245                      250                      255
200   Leu Trp Asp Ile Tyr Asn Thr Asp Glu Tyr Val Ala Tyr Pro Asp Asp
201           260                      265                      270
203   Glu Leu Gln Val Ala Ser Thr Ile Val Asp Val Ser Asn Gly Lys Val
204           275                      280                      285
206   Ile Ala Gln Leu Gly Ala Arg His Gln Ser Ser Asn Val Ser Phe Gly
207           290                      295                      300
209   Ile Asn Gln Ala Val Glu Thr Asn Arg Asp Trp Gly Ser Thr Met Lys
210           305                      310                      315                      320
212   Pro Ile Thr Asp Tyr Ala Pro Ala Leu Glu Tyr Gly Val Tyr Asp Ser
213           325                      330                      335
215   Thr Ala Thr Ile Val His Asp Glu Pro Tyr Asn Tyr Pro Gly Thr Asn
216           340                      345                      350
218   Thr Pro Val Tyr Asn Trp Asp Arg Gly Tyr Phe Gly Asn Ile Thr Leu
219           355                      360                      365
221   Gln Tyr Ala Leu Gln Gln Ser Arg Asn Val Pro Ala Val Glu Thr Leu
222           370                      375                      380
224   Asn Lys Val Gly Leu Asn Arg Ala Lys Thr Phe Leu Asn Gly Leu Gly
225           385                      390                      395                      400
227   Ile Asp Tyr Pro Ser Ile His Tyr Ser Asn Ala Ile Ser Ser Asn Thr
228           405                      410                      415
230   Thr Glu Ser Asp Lys Lys Tyr Gly Ala Ser Ser Glu Lys Met Ala Ala
231           420                      425                      430
233   Ala Tyr Ala Ala Phe Ala Asn Gly Gly Thr Tyr Tyr Lys Pro Met Tyr
234           435                      440                      445
236   Ile His Lys Val Val Phe Ser Asp Gly Ser Glu Lys Glu Phe Ser Asn
237           450                      455                      460
239   Val Gly Thr Arg Ala Met Lys Glu Thr Thr Ala Tyr Met Met Thr Asp
240           465                      470                      475                      480
242   Met Met Lys Thr Val Leu Thr Tyr Gly Thr Gly Arg Asn Ala Tyr Leu
243           485                      490                      495
245   Ala Trp Leu Pro Gln Ala Gly Lys Thr Gly Thr Ser Asn Tyr Thr Asp

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246          500          505          510
248      Glu Glu Ile Glu Asn His Ile Lys Thr Ser Gln Phe Val Ala Pro Asp
249          515          520          525
251      Glu Leu Phe Ala Gly Tyr Thr Arg Lys Tyr Ser Met Ala Val Trp Thr
252          530          535          540
254      Gly Tyr Ser Asn Arg Leu Thr Pro Leu Val Gly Asn Gly Leu Thr Val
255          545          550          555          560
257      Ala Ala Lys Val Tyr Arg Ser Met Met Thr Tyr Leu Ser Glu Gly Ser
258          565          570          575
260      Asn Pro Glu Asp Trp Asn Ile Pro Glu Gly Leu Tyr Arg Asn Gly Glu
261          580          585          590
263      Phe Val Phe Lys Asn Gly Ala Arg Ser Thr Trp Asn Ser Pro Ala Pro
264          595          600          605
266      Gln Gln Pro Pro Ser Thr Glu Ser Ser Ser Ser Ser Asp Ser Ser
267          610          615          620
269      Thr Ser Gln Ser Ser Ser Thr Thr Pro Ser Thr Asn Asn Ser Thr Thr
270          625          630          635          640
272      Thr Asn Pro Asn Asn Asn Thr Gln Gln Ser Asn Thr Thr Pro Asp Gln
273          645          650          655
275      Gln Asn Gln Asn Pro Gln Pro Ala Gln Pro
276          660          665

278 (2) INFORMATION FOR SEQ ID NO: 3:
280     (i) SEQUENCE CHARACTERISTICS:
281         (A) LENGTH: 1714 base pairs
282         (B) TYPE: nucleic acid
283         (C) STRANDEDNESS: double
284         (D) TOPOLOGY: linear
288     (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3:
290 AAATTACAAT ACGGACTATG AATTGACCTC TGGAGAAAAA TTACCTCTTC CTAAAGAGAT      60
292 TTCAGGTTAC ACTTATATTG GATATATCAA AGAGGGAAAA ACGACTTCTG AGTCTGAAGT      120
294 AAGTAATCAA AAGAGTTCAG TTGCCACTCC TACAAAACAA CAAAAGGTGG ATTATAATGT      180
296 TACACCGAAT TTTGTAGACC ATCCATCAAC AGTACAAGCT ATTCAGGAAC AAACACCTGT      240
298 TTCTTCAACT AAGCCGACAG AAGTTCAAGT AGTTGAAAAA CCTTCTCTA CTGAATTAAT      300
300 CAATCCAAGA AAAGAAGAGA AACAATCTTC AGATTCTCAA GAACAATTAG CCGAACATAA      360
302 GAATCTAGAA ACGAAGAAAG AGGAGAAGAT TTCTCCAAAA GAAAAGACTG GGGTAAATAC      420
304 ATTAAATCCA CAGGATGAAG TTTTATCAGG TCAATTGAAC AAACCTGAAC TCTTATATCG      480
306 TGAGGAAACT ATGGAGACAA AAATAGATTT TCAAGAAGAA ATTCAAGAAA ATCCTGATTT      540
308 AGCTGAAGGA ACTGTAAGAG TAAAACAAGA AGGTAAATTA GGTAAGAAAG TTGAAATCGT      600
310 CAGAATATTC TCTGTAAACA AGGAAGAAGT TTCGCGAGAA ATTGTTTCAA CTTCACGAC      660
312 TGCGCCTAGT CCAAGAATAG TCGAAAAAGG TACTAAAAAA ACTCAAGTTA TAAAGGAACA      720
314 ACCTGAGACT GGTGTAGAAC ATAAGGACGT ACAGTCTGGA GCTATTGTTG AACCCGCAAT      780
316 TCAGCCTGAG TTGCCCGAAG CTGTAGTAAG TGACAAAGGC GAACCAGAAG TTCAACCTAC      840
318 ATTACCCGAA GCAGTTGTGA CCGACAAAGG TGAGACTGAG GTTCAACCAG AGTCGCCAGA      900
320 TACTGTGGTA AGTGATAAAG GTGAACCAGA GCAGGTAGCA CCGCTTCCAG AATATAAGGG      960
322 TAATATTGAG CAAGTAAAC CTGAACTCC GGTGAGAAG ACCAAAGAAC AAGGTCCAGA     1020
324 AAAAAGTAA GAAGTTCCAG TAAAACCAAC AGAAGAAACA CCAGTAAATC CAAATGAAGG     1080
326 TACTACAGAA GGAACCTCAA TTCAAGAAGC AGAAAATCCA GTTCAACCTG CAGAAGAATC     1140
328 AACACGAAT TCAGAGAAAG TATCACCAGA TACATCTAGC AAAAATACTG GGAAGTGTC     1200
330 CAGTAATCCT AGTGATTCTG CAACCTCAGT TGGAGAATCA AATAAACAG AACATAATGA     1260

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```

332 CTCTAAAAAT GAAATTCAG AAAAACTGT AGAAGAAGTT CCAGTAAATC CAAATGAAGG 1320
334 CACAGTAGAA GGTACCTCAA ATCAAGAAAC AGAAAAACCA GTTCAACCTG CAGAAGAAAC 1380
336 ACAAACAAAC TCTGGGAAAA TAGCTAACGA AAATACTGGA GAAGTATCCA ATAAACCTAG 1440
338 TGATTCAAAA CCACCAAGTTG AAGAATCAAA TCAACCAGAA AAAAACGGAA CTGCAACAAA 1500
340 ACCAGAAAAT TCAGGTAATA CAACATCAGA GAATGGACAA ACAGAACCAG AACCATCAAA 1560
342 CGGAAATTCA ACTGAGGATG TTTCAACCGA ATCAAACACA TCCAATTCAA ATGGAAACGA 1620
344 AGAAATTAAA CAAGAAAATG AACTAGACCC TGATAAAAAG GTAGAAGAAC CAGAGAAAAC 1680
346 ACTTGAATTA AGAAATGTTT CCGACCTAGA GTTA 1714
348 (2) INFORMATION FOR SEQ ID NO: 4:
350 (i) SEQUENCE CHARACTERISTICS:
351 (A) LENGTH: 571 amino acids
352 (B) TYPE: amino acid
353 (C) STRANDEDNESS: single
354 (D) TOPOLOGY: linear
356 (ii) MOLECULE TYPE: protein
359 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4:
361 Asn Tyr Asn Thr Asp Tyr Glu Leu Thr Ser Gly Glu Lys Leu Pro Leu
362 1 5 10 15
364 Pro Lys Glu Ile Ser Gly Tyr Thr Tyr Ile Gly Tyr Ile Lys Glu Gly
365 20 25 30
367 Lys Thr Thr Ser Glu Ser Glu Val Ser Asn Gln Lys Ser Ser Val Ala
368 35 40 45
370 Thr Pro Thr Lys Gln Gln Lys Val Asp Tyr Asn Val Thr Pro Asn Phe
371 50 55 60
373 Val Asp His Pro Ser Thr Val Gln Ala Ile Gln Glu Gln Thr Pro Val
374 65 70 75 80
376 Ser Ser Thr Lys Pro Thr Glu Val Gln Val Val Glu Lys Pro Phe Ser
377 85 90 95
379 Thr Glu Leu Ile Asn Pro Arg Lys Glu Glu Lys Gln Ser Ser Asp Ser
380 100 105 110
382 Gln Glu Gln Leu Ala Glu His Lys Asn Leu Glu Thr Lys Lys Glu Glu
383 115 120 125
385 Lys Ile Ser Pro Lys Glu Lys Thr Gly Val Asn Thr Leu Asn Pro Gln
386 130 135 140
388 Asp Glu Val Leu Ser Gly Gln Leu Asn Lys Pro Glu Leu Leu Tyr Arg
389 145 150 155 160
391 Glu Glu Thr Met Glu Thr Lys Ile Asp Phe Gln Glu Glu Ile Gln Glu
392 165 170 175
394 Asn Pro Asp Leu Ala Glu Gly Thr Val Arg Val Lys Gln Glu Gly Lys
395 180 185 190
397 Leu Gly Lys Lys Val Glu Ile Val Arg Ile Phe Ser Val Asn Lys Glu
398 195 200 205
400 Glu Val Ser Arg Glu Ile Val Ser Thr Ser Thr Thr Ala Pro Ser Pro
401 210 215 220
403 Arg Ile Val Glu Lys Gly Thr Lys Lys Thr Gln Val Ile Lys Glu Gln
404 225 230 235 240
406 Pro Glu Thr Gly Val Glu His Lys Asp Val Gln Ser Gly Ala Ile Val
407 245 250 255
409 Glu Pro Ala Ile Gln Pro Glu Leu Pro Glu Ala Val Val Ser Asp Lys

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VERIFICATION SUMMARY
PATENT APPLICATION: US/09/765,271

DATE: 03/16/2001
TIME: 17:53:04

Input Set : N:\paola\09765271.txt
Output Set: N:\CRF3\03162001\I765271.raw

L:33 M:220 C: Keyword misspelled or invalid format, [(A) APPLICATION NUMBER:]
L:34 M:220 C: Keyword misspelled or invalid format, [(B) FILING DATE:]
L:54 M:220 C: Keyword misspelled or invalid format, [(ix) TELECOMMUNICATION INFORMATION:]
L:815 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:10
L:2577 M:111 C: (47) String data converted to upper case,
M:111 Repeated in SeqNo=41
L:2809 M:111 C: (47) String data converted to upper case,
M:111 Repeated in SeqNo=45
L:2849 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:46
L:2906 M:111 C: (47) String data converted to upper case,
M:111 Repeated in SeqNo=47
L:3236 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:52
L:3551 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:56
L:3733 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:58
L:3736 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:58
L:4217 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:66
L:4295 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:66
L:4858 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:74
L:4994 M:111 C: (47) String data converted to upper case,
M:111 Repeated in SeqNo=75
L:5062 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:76
L:5251 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:80
L:5284 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:80
L:5417 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:82
L:6864 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:106
L:6867 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:106
L:6879 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:106
L:6894 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:106
L:6935 M:111 C: (47) String data converted to upper case,
M:111 Repeated in SeqNo=107
L:7466 M:111 C: (47) String data converted to upper case,
L:7612 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:118
L:7792 M:111 C: (47) String data converted to upper case,
L:7886 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:120
L:10026 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:160
L:10147 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:162
L:10603 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:172
L:10606 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:172
L:10609 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:172
L:10829 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:176
L:11704 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:194
L:13925 M:111 C: (47) String data converted to upper case,